

FIG. 1

ccggaattcccggtcgacccacgcgtccggccccccattcaagaagccgctcagctatcccgccagcacagggcgc  
 ccggcgcgccctcggagcgcaagttcctcgcttctcctgcccgcctcgtgggcattatgcgccaagcagccgagccccagtcctc  
 5 ctcctcctcctgctcctccggctcctcctcgggcccagcggtcagctctcggcagggcggtgctcagccgagcgcagac  
 gggacccctcgagcgagacctcagcgactcctaaagtcaaaagtggcgggcgccggggtccgcgctctccacggcgctg  
 cctcgctcgccgcccagccaaggagggcaggagggaggggggtggggcagcgaggaggggtgggaagcaccatgcagtttg  
 taccctggccacactgctaacgctcctggtgcggaacctggccgagatggggagcccagacgcgcggcggtgcgcaaggac  
 aggtgcacccgaggcaagtgaattattagagacctgagcgaatacgaaatcgtgtctccatccgagtgaaacgctctcggaga  
 10 accctttccacgaacgtccacttcaaaagaacgcgagcggagcattaactctgccactgacccctggcctgccttcgctcctcct  
 ctctcctcctacctcctccaggcgcttaccgctctctgcttcggccagcagtttctatttaattctaccgccaatgccgga  
 ttatcgctccactgttactgtcacccctcctcggaacgcccgggtgaatcagaccaagttttattccgaagaggaagcggaact  
 caagcactgtttctacaaaggctatgtcaataccaactccgagcacacggccgtcatcagcctctgctcaggaatgctgggcacat  
 tccggctctcatgatggggattattttattgaaccactacagtctatggatgaacaagaagatgaagaggaacaaaaaacccac  
 15 atcatttataggcgagcgccccccagagagagccctcaacaggaaggcatgcatgtgacacctcagaacacaaaaataggcacag  
 taaagacaagaagaaaaccagagcaagaaaatggggagaaaggattaacctggctggtgacgtagcagcattaaacagcggttag  
 caacagaggcattttctgcttatggttaataagacggacaacacagaagaaaaggaccacagaaggacaaaacgtttttatcc  
 tatccacggtttgtagaagtcttggtggtgagacacagaatggtttcataccatggagaaaaccttcaacactatattttaac  
 tttaatgtcaattgtagcctctatctataaagacccaagtattggaaatttaattaatattgttattgtgaacttaattgtgattc  
 20 ataataagacaggtatggccttccatctcttttaattgtcagacaacattaaaaaacttttgccagtggtgagcattcgaagaacagt  
 ccaggtggaatccatcatgatactgctgttctcttaacaagacaggatatctgcagagctcacgacaaatgtgataccttaggcct  
 ggctgaactgggaaccattttgtgatccctatagaagctgttctattagtgaagatagtggttagtgacagcttttacgatcgcc  
 atgagctgggcatgtgtttaacatgcctcatgatgacaacaacaaatgtaagaagaaggagtttaagagctcccagcatgtcatg  
 gctccaacactgaactctacaccaacccctggatgtggtcaaaagtgtagtcgaaaatatatcactgagtttttagacactggtta  
 25 tggcgagtgtttgcttaacgaacctgaatccagacctaccctttgctgtccaactgccaggcatcctttacaacgtgaataaac  
 aatgtgaattgatttttgaccaggttctcaggtgtgccatataatgatgcagtgacagcggtctggtgcaataacgtcaatgga  
 gtacacaaaaggctgcggactcagcacacacctgggcccagtgaggagtgagcgtggaagcactgcaagtatggattttg  
 tgttcccaagaaatggatgtccccgtgacagatggatccctggggaagtggagtcctttggaacctgctccagaacatgtggag  
 ggggcatcaaaacagccattcgagagtgaacagaccagaacaaaaaatggtggaataactgtgtaggacgtagaatgaaattt  
 30 aagtcctgcaacacggagccatgtctcaagcagaagcgagactccgagatgaacagtggtcactttgacgggaagcattttta  
 catcaacggtctgcttccaatgtgcgctgggtccctaaatacagtggaattctgatgaaggaccggtgcaagttgtctgcagag  
 tggcagggaaacacagcctactatcagcttcgagacagagtgatagatggaactccttggtggccaggacacaaatgatctgtgct  
 cagggcctttgcccgaagctggatgcgatcatgttttaactcaaaagcccggagagataaatgtggggtttgtggtggcgataa  
 35 tcttcatgcaaaacagtggtgaggaacatttaatacagtagcattatggttacaatactgtggtccgaattccagctggtgctacca  
 atattgatgtggtgagcagcagtttctcaggggaaacagacgatgacaactacttagctttatcaagcagtaaaagtgaaattcttg  
 ctaaatggaactttgtgtgcacatggccaaaagggaattcgcattgggaatgctgtggttagtagtacagtggtccgagactgc  
 cgtagaaagaattaactcaacagatcgattagcaagaacttttgcttcaggtttgtcggtgggaaagtgtacaacccccgatg  
 tacgctattctttcaatattccaattgaagataaacctcagcagttttactggaacagtcagtggtccatggcaagcatgcagtaaa  
 40 cctgccaaggggaacggaaacgaaaactgtttgaccagggaatctgatcagcttactgtttctgatcaaatgagtgatgcggt  
 gccccagcctggacacattactgaacctgtggtacagactgtgacctgaggtggcatgttgccagcaggagtgaaatgtagtgcc  
 agtggtggttgggttaccgcacattggacatctactgtgcaaatatagcaggctggatgggaagactgagaaggttgatgatggt  
 ttttgagcagccatcccaaaccagcaaccgtgaaaaatgctcaggggaatgtaacacgggtggctggcgctattctgcctggac  
 tgaatgttcaaaaagctgtgacggtgggacccagaggagaagggtattttgtgtcaatacccgaaatgatgtactggatgacagca  
 aatgcacacatcaagagaaagtaccattcagaggtgcagtgagttccctgtccacagtggaatctggagactggtcagagtg  
 45 ttggtcacctgtggaaggccataagcaccgccaggtctggtgacagtttgggtgaagatcgattaaatgatagaatgtgtgaccc

FIG. 1 "252450"

tgagaccaagccaacatctatgcagacttgtcagcagccggaatgtgcatcctggcagggcgggtccctggggacagtgcagtgtca  
cttgtggacagggataccagctaagagcagtgaaatgcatcattgggacttatatgtcagtggttagatgacaatgactgtaatgca  
gcaactagaccaactgataccaggactgtgaattacatcatgtcatcctccccagctgccccggaacgaggagaagcacata  
cagtgccaccaagaaccagtggcgatttgggtcttggaccccatgctcagccacttgtgggaaggtacccggatgagatacgtca  
5 gctgccgagatgagaatggctctgtggctgacgagagtgcctgtgctaccctgcctagaccagtggcaaggaagaatgttctgtg  
acaccctgtgggcaatggaaggccttggactggagctcttgtctgtgacctgtgggcaaggtagggaacccggcaagtgtgtg  
tgtcaactacagtgaccacgtgatcgatcggagtgtgtgaccaggattatatccagaaactgaccaggactgttccatgtcac  
catgccctcaaaggacccagacagtggcttagctcagcacccttccaaaatgaggactatcgtccccggagcgccagccccagc  
cgcacccatgtgctcgggtggaaccagtggaactggccctggggagcatgttccagtacctgtgtggcgatcccagcggcg  
10 tgttgttgtatgtcaggatgaaaatggataccgcaaacgactgtgtggagagaataaaacctgatgagcaaaagacctgtgaat  
ccggcccttgtcctcagtggttattggcaactggggagagtgcactaagctgtgtgtggaggcataagaacaagactggtgtc  
tgtcagcgggtccaacggtgaacggtttccagatttgagctgtgaaattcttgataaacctcccgatcgtgagcagtgtaacacaca  
tgcttgtccacacgacgctgcattggagtactggcccttgagctcgtgttctgtctcttgtgtgcagggcataaacaacgaaatg  
tttactgcatggcaaaagatggaagccatttagaaaatgattactgtaagcacctggctaagccacatgggcacagaaagtgccga  
15 ggaggaagatgccccaaatggaagctggcgcttggagtgcagtgcctgtgtcctgtgtggccgaggcgtacagcagaggcatgtggg  
ctgtcagatcggaacacacaaaaatagccagagagaccgagtcaaccatacaccagaccggagtgcgaacgcgactgccaaggcc  
cacggtgtccctctacacttggagggcagaggaatggcaagaatgcaccaagacctgcggcgaaggctccaggtaccgcaagggtg  
gtgtgtgtggatgacaacaaaaacgaggtgcatggggcacgctgtgacgtgagcaagcggccggtggaccgtgaaagctgtagt  
gcaaccctgcgagtatgtctggatcacaggagaatggtcagaggtaccgtcctgggaactgtaaccatcgtcagctcagccatggc  
20 ctgagagtggcagagggatgagtggagggatgagtgcaggaatgtgggagacttgaggctaccgcgccgatttgcactgtgaact  
gtgtgttttctgacaagtcctcagcttcccaagctagaattccttgtatgcaaagcgggagagatgtaagagatggtctctaagt  
cccttcaggtctacattctgtgattcaccttgatgtcctattggcataaagaagaaattattacaggggctgcaaaactcataggat  
gctgtgaggtgcctgaagacagttaagtataagaaaatattgtagtccagggatacaacaaggagagatggcaactgtgacaaac  
tagcacatgctgtgtgaagggagcagaatctcttccactccagctgtggccatgcagaaatgtgggtctagcgttaccagacctgat  
25 ttttcaagagaggctaaaaatctggactagtatgtgagatttcctaactgaaaatgggggctgaaatttttggttttaaacatt  
gtaaggggcaacaaaccccttcatgaaccagatgtgtgtgcctgtttaacaaacagcttcagaggaagaaaataattttctat  
aatatccgaagtatctcaagtac

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

FIG. 2

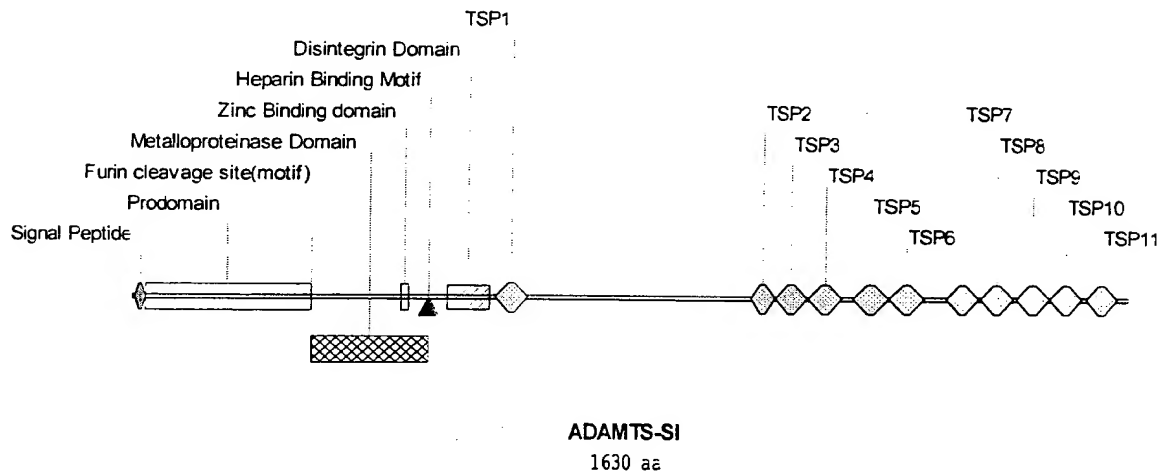
5 atdpwpa fasssssstssqahyr lsa fgqqlfnltanagfiaplftvtllgtpgvnqt kfyseeeaelkhcfykygvntnsehta  
 vislcs gmlgtfrshdgd yfieplqsmdegedeeeqn kphiiyr rsapqrepstgr hacdtsehknr hskdkkktrarkwgerinl  
 agdvaal nsglateaf saygnktdntrekr thrtrkrlsfypr fvevlvvadnrmv syhgenlqh yiltlmsivasiykdpsign  
 inivivn livihneq dqpssisfnaqttlknfcqwqhs knspggihdta vlltrqdicrahdkcdtlglaelgticdpyrscsise  
 ds glstaftia helghvf nmp hddnnkckeegvkspqhvm aptlnfytnp mwmwskcsrkyitefldtgygecllnepesrpylpv  
 10 qlpgily nvnkqcelif gpgsqvc pmmqcr rrlwcn nvnvgvhkgcrtqhtp wadgtecepgkhckygfvcvkemdv pvt dgs wgs w  
 spfgtcs rtcgggiktai re cnrpepknggky cvgrmkfks cntepcl kqkrdrf deqcahfdgkhfningllpnvrwvpky sgi  
 lmkdrckl fcrvagntayyqlrdrvidgt pcpqgd tndicvqglcrqagcdhvl nlskarrdkcgvcggdns scktvagt fntvhygy  
 ntvr ipagatnidvrqhsf sgetddnyl alssskgefl lngnfvtmakreir igrignavveys gsetaver instdrieqelllq  
 vlsvgklyn pdvrysfnipiedk pqqfywnshg pwpqacskpcqgerkrklvctresdqltvsd qrcdr lppgghitepcgt dcdlr  
 15 whvasr secsaqcglgyrtldiycakys rldgktekvddgfcsshpkpsnre kcsgecntggwrysawtecskscdgg tqr rraic  
 vntrndv lddskcthqekvtiqrcse fpcpqwksgdwseclvtcgkghkhrqvwqc qgedrlndrmcdpetkptsmgtcq qpecas  
 wqagpwwqcs vtcgggyqlravkciigt ymsvddndcnaatrptdtqdcelpschpppaapetrstysaprtqwrfgswtpcsa  
 tcgkgtrmryvscrdengsvadesacatlprpvakeecsvtpcgqwkaldwsscsvtcgqgratr qvmcnysdhvidrsecdqdy  
 ipetdqdcsm spcpqrtpds glaqhpfqnedyrpr saspsrthvlggnqwrtpgwgacsstcaggsqrrvvvcqdengytandcve  
 20 rikpdegracesgpcpqwaygnwgectklcgggirtrlvvcqrsngerfpdlsceildkppdre qc nthacphdaawstgpwsscs  
 vscgrghkqrnvycmakdgshlesdyckhlakphghrkr cggrcpkwkagawsqcs vscgrgvqqrhvgcqigthkiaretecnpy  
 trpeserdcqgprcplytwraeewgectktcgegsr yrkvvcvddnkn evhgarcdvskrpvdrescslqpceyvwtigewsevp  
 wel\*

25

**Fig. 3**

**Domain structure of ADAMTS-SI**

Signal peptide (1-18), Prodomain (19-287), Furin cleavage site (288), Metalloproteinase domain (289-478), Zinc binding motif (434-446), Heparin binding motif (478-482), Disintegrin domain (509-578), Thrombospondin motif (589-642), Spacer region (643-1014), Thrombospondin submotifs (1001-1053, 1056-1108, 1111-1165, 1186-1239, 1240-1295, 1332-1383, 1386-1439, 1445-1500, 1501-1554, 1559-1612)



B

```

1  CCGGAATTCC CGGGTCGACC CACGCGTCCG GCCCCCATT CAAGAAGCCG CTCAGCTATC
   GGCCTTAAGG GCCCAGCTGG GTGCGCAGGC CGGGGGGTAA GTTCTTCGGC GAGTCGATAG

61  CCGGCCAGCA CAGGGCGCCC GGCGCGCCTC GGAGCGCAAG TTCCTCGCCT TCTCTGCCC
   GGCCGGTCGT GTCCCGCGGG CCGCGCGGAG CCTCGCGTTC AAGGAGCGGA AGAGGACGGG

121 GCTCGCTGGG CATTATGCGG CCAAGCAGCC GAGCCCCAGT CCTCCTCCTC CTCCTGCTCC
   CGAGCGACCC GTAATACGCC GGTTCGTCGG CTCGGGGTCA GGAGGAGGAG GAGGACGAGG

181 TCCGGCTCCT CTGCGGCCC GAGCGGCTCA GCTCTCGGCA GGCGGCGGCG TTGCTCAGCC
   AGGCCGAGGA GGACGCCGGG CTCGCGGAGT CGAGAGCCGT CCGCCGCGCC AACGAGTCGG

241 GAGCGCAGAC GGGACCCTCG CAGCGAGACC TCAGCGACTC CTAAGTCAA AAGTTGGCGG
   CTCGCGTCTG CCCTGGGAGC GTCGCTCTGG AGTCGCTGAG GATTTCAGTT TTCAACCGCC

301 CGGGCGCCGG GCTCCGCGCG CTCTCCACGG CCGCTGCCTC GCGTCGCCGC CGCAGCCAAG
   GCCCGCGGCC CGAGGCGCGC GAGAGGTGCC GCGACGGAG CGCAGCGGCG GCGTCGGTTC

+2                                     M Q F
                                     Start met
                                     ===
                                     Kozak consensus
                                     =====
                                     Signal peptide
                                     =====

361 GAGGGCAGGA GGGAGGGGGG TGGGGGCAGC GGAGGGAGGG GTGGGAAGCA CCATGCAGTT
   CTCCGTCCT CCCTCCCCC ACCCCCGTCG CTTCCCTCCC CACCCTTCGT GGTACGTCAA

+2  V S W  A T L L T L L  V R D L A E M G S P
                                     signal peptide cleavage site
                                     =

                                     Signal peptide                               Prodomain
=====
421 TGTATCTGG GCCACACTGC TAACGCTCCT GGTGCGGGAC CTGGCCGAGA TGGGGAGCCC
   ACATAGGACC CGGTGTGACG ATTGCGAGGA CCACGCCCTG GACCGGCTCT ACCCTCGGG

+2  D A A  A A V R  K D R  L H P  R Q V K  L L E
                                     Prodomain
=====

481 AGACGCCGCG GCGGCGTGC GCAAGGACAG GCTGCACCCG AGGCAAGTGA AATTATTAGA
   TCTGCGGCGC CGCCGGCAGC CGTTCCTGTC CGACGTGGGC TCGTTCACT TTAATAATCT

+2  T L S  E Y E I  V S P  I R V  N A L G  E P F
                                     Prodomain
=====

541 GACCCTGAGC GAATACGAAA TCGTGTCTCC CATCCGAGTG AACGCTCTCG GAGAACCCTT
   CTGGGACTCG CTTATGCTTT AGCACAGAGG GTAGGCTCAC TTGCGAGAGC CTCTTGGGAA

+2  P T N  V H F K  R T R  R S I  N S A T  D P W
                                     Prodomain
=====

601 TCCCACGAAC GTCCACTTCA AAAGAACGCG ACGGAGCATT AACTCTGCCA CTGACCCCTG

```

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100

```

+2 P A F A S S S S S S T S S Q A H Y R L S
                                         Prodomain.
=====
661 GCCTGCCTTC GCCTCCTCCT CTCCTCCTC TACCTCCTCC CAGGCGCATT ACCGCCTCTC
    CGGACGGAAG CGGAGGAGGA GAAGGAGGAG ATGGAGGAGG GTCCGCGTAA TGGCGGAGAG

+2 A F G Q Q F L F N L T A N A G F I A P I
                                         Prodomain.
=====
721 TGCCTTCGGC CAGCAGTTTC TATTTAATCT CACCGCCAAT GCCGGATTTA TCGCTCCACT
    ACGGAAGCCG GTCGTCAAAG ATAAATTAGA GTGGCGGTGA CGGCCTAAAT AGCGAGGTGA

+2 F T V T L L G T P G V N Q T K F Y S E E
                                         Prodomain.
=====
781 GTTCACTGTC ACCCTCCTCG GGACGCCCGG GGTGAATCAG ACCAAGTTTT ATTCCGAAGA
    CAAGTGACAG TGGGAGGAGC CTGCGGGGCC CCACTTAGTC TGGTCAAAA TAAGGCTTCT

+2 E A E L K H C F Y K G Y V N T N S E H T
                                         Prodomain
=====
841 GGAAGCGGAA CTCAAGCACT GTTCTACAA AGGCTATGTC AATACCAACT CCGAGCACAC
    CCTTCGCCTT GAGTTCGTGA CAAAGATGTT TCCGATACAG TTATGGTTGA GGCTCGTGTC

+2 A V I S L C S G M L G T F R S H D G D Y
    Prodomain
=====
901 GGCCGTCATC AGCCTCTGCT CAGGAATGCT GGGCACATTC CGGTCTCATG ATGGGGATTA
    CCGGCAGTAG TCGGAGACGA GTCCTTACGA CCCGTGTAAG GCCAGAGTAC TACCCCTAAT

+2 F I E P L Q S M D E Q E D E E E Q N K P
    Prodomain
=====
961 TTTTATTGAA CCACTACAGT CTATGGATGA ACAAGAAGAT GAAGAGGAAC AAAACAAACC
    AAAATAACTT GGTGATGTCA GATACCTACT TGTCTTCTA CTCTCCTTG TTTTGTGTTG

+2 H I I Y R R S A P Q R E P S T G R H A C
    Prodomain
=====
1021 CCACATCATT TATAGGCGCA GCGCCCCCA GAGAGAGCCC TCAACAGGAA GGCATGCATG
    GGTGTAGTAA ATATCCGCGT CGCGGGGGGT CTCTCTCGGG AGTTGTCCTT CCGTACGTAC

+2 D T S E H K N R H S K D K K K T R A R K
    Prodomain
=====
1081 TGACACCTCA GAACACAAAA ATAGGCACAG TAAAGACAAG AAGAAAACCA GAGCAAGAAA
    ACTGTGGAGT CTTGTGTTTT TATCCGTGTC ATTTCTGTTT TTCTTTTGGT CTCGTTCTTT

+2 W G E R I N L A G D V A A L N S G L A T
    Prodomain
=====
1141 ATGGGGAGAA AGGATTAACC TGGCTGGTGA CGTAGCAGCA TTAAACAGCG GCTTAGCAAC
    TACCCCTCTT TCCTAATTGG ACCGACCACT GCATCGTCGT AATTGTGCGC CGAATCGTTG

```

```

-2  E A F S A Y G N K T D N T R E K R T H F
    Prodomain.
=====
1201 AGAGGCATTT TCTGCTTATG GTAATAAGAC GGACAACACA AGAGAAAAGA GGACCCACAG
    TCTCCGTAAA AGACGAATAC CATTATCTCG CCTGTTGTGT TCTCTTTTCT CCTGGGTGTC

+2  R T K R F L S Y P R F V E V L V V A D N
    Furin Cleavage site

    Prodomain.                               Metalloproteinase domain
=====
1261 AAGGACAAAA CGTTTTTAT CCTATCCACG GTTGTAGAA GTCTTGGTGG TGGCAGACAA
    TTCTGTITT GCAAAAAATA GGATAGGTGC CAAACATCTT CAGAACCACC ACCGTCTGTT

+2  R M V S Y H G E N L Q H Y I L T L M S I
    Metalloproteinase domain
=====
1321 CAGAATGGTT TCATACCATG GAGAAAACCT TCAACACTAT ATTTAACTT TAATGTCAAT
    GTCTTACCAA AGTATGGTAC CTCTTTTGA AGTTGTGATA TAAAATTGAA ATTACAGTTA

+2  V A S I Y K D P S I G N L I N I V I V N
    Metalloproteinase domain
=====
1381 TGTAGCCTCT ATCTATAAG ACCCAAGTAT TGGAAATTTA ATTAATATTG TTATTGTGAA
    ACATCGGAGA TAGATATTTC TGGGTTTATA ACCTTTAAAT TAATTATAAC AATAACACTT

+2  L I V I H N E Q D G P S I S F N A Q T T
    Metalloproteinase domain
=====
1441 CTTAATTGTG ATTCATAATG AACAGGATGG GCCTTCCATA TCTTTTAATG CTCAGACAAC
    GAATTAACAC TAAGTATTAC TTGTCCTACC CGGAAGGTAT AGAAAATTAC GAGTCTGTGG

+2  L K N F C Q W Q H S K N S P G G I H H D
    Metalloproteinase domain
=====
1501 ATTAAAAAAC TTTTGCCAGT GGCAGCATTC GAAGAACAGT CCAGGTGGAA TCCATCATGA
    TAATTTTTTG AAAACGGTCA CCGTCGTAAG CTTCTGTGCA GGTCCACCTT AGGTAGTACT

+2  T A V L L T R Q D I C R A H D K C D T I
    Metalloproteinase domain
=====
1561 TACTGCTGTT CTCTTAACAA GACAGGATAT CTGCAGAGCT CACGACAAAT GTGATACCTT
    ATGACGACAA GAGAATTGTT CTGTCCTATA GACGICTCGA GTGCTGTTTA CACTATGGAA

+2  G L A E L G T I C D P Y R S C S I S E L
    Metalloproteinase domain
=====
1621 AGGCCTGGCT GAACTGGGAA CCATTGTGTA TCCCTATAGA AGCTGTTCTA TTAGTGAAGA
    TCCGGACCGA CTTGACCCTT GGTAAACACT AGGGATATCT TCGACAAGAT AATCACTTC

```





```

V P V T D G S W G S W S F F G T C S R T
Disintegrin domain TSP1
=====
2161 TGTCCCCGTG ACAGATGGAT CCTGGGGAAG TTGGAGTCCC TTGGAACTT GCTCCAGAAC
ACAGGGGGCAC TGCTACCTA GGACCCCTTC AACCTCAGGG AAACCTTGGA CGAGGTCTTG

+2 C G G G I K T A I R E C N R P E P K N G
TSP1
=====
2221 ATGTGGAGGG GGCATCAAAA CAGCCATTTC AGAGTGCAAC AGACCAGAAC CAAAAATGG
TACACCTCCC CCGTAGTTTT GTCGGTAAGC TCTCACGTTG TCTGGTCTTG GTTTTTTACC

+2 G K Y C V G R R M K F K S C N T E P C L
TSP1 Spacer Region
=====
2281 TGGAAAATAC TGGTAGGAC GTAGAATGAA ATTTAAGTCC TGCAACACGG AGCCATGTCT
ACCTTTTATG ACACATCCTG CATCTTACTT TAAATTCAGG ACGTTGTGCC TCGGTACAGA

+2 K Q K R D F R D E Q C A H F D G K H F N
Spacer Region
=====
2341 CAAGCAGAAG CGAGACTTCC GAGATGAACA GTGTGCTCAC TTGACGGGA AGCATTTTAA
GTTCGTCTTC GCTCTGAAGG CTCTACTTGT CACACGAGTG AAACCTGCCCT TCGTAAAATT

+2 I N G L L P N V R W V P K Y S G I L M K
Spacer Region
=====
2401 CATCAACGGT CTGCTTCCCA ATGTGCGCTG GGTCCCTAAA TACAGTGGAA TTCTGATGAA
GTAGTTGCCA GACGAAGGGT TACACGCGAC CCAGGGATTT ATGTCACCTT AAGACTACTT

+2 D R C K L F C R V A G N T A Y Y Q L R D
Spacer Region
=====
2461 GGACCGGTGC AAGTTGTCT GCAGAGTGGC AGGGAACACA GCCTACTATC AGCTTCGAGA
CCTGGCCACG TTCAACAAGA CGTCTCACC GTCCTTGTGT CGGATGATAG TCGAAGCTCT

+2 R V I D G T P C G Q D T N D I C V Q G L
Spacer Region
=====
2521 CAGAGTGATA GATGGAATC CTGTGGCCA GGACACAAAT GATATCTGTG TCCAGGGCCT
GTCTCACTAT CTACCTTGAG GAACACCGGT CCTGTGTTTA CTATAGACAC AGGTCCCGGA

+2 C R Q A G C D H V L N S K A R R D K C G
Spacer Region
=====
2581 TTGCCGGCAA GCTGGATGCG ATCATGTTTT AAACCTCAAAA GCCCGGAGAG ATAAATGTGG
AACGGCCGTT CGACCTACGC TAGTACAAAA TTGAGTTTT CGGGCCTCTC TATTACACC

+2 V C G G D N S S C K T V A G T F N T V H
Spacer Region
=====
2641 GGTITGTGGT GGCATAATT CTTCATGCAA AACAGTGGCA GGAACATTTA ATACAGTACA
CCAAACACCA CCGCTATTAA GAAGTACGTT TTGTCACCGT CCTGTAAAT TATGTCATGT

```

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

+2 Y G Y N T V V R I P A G A T N I D V R C  
Spacer Region

=====  
2701 TTATGGTTAC AATACTGTGG TCCGAATTCC AGCTGGTGCT ACCAATATTG ATGTGCGGCA  
AATACCAATG TTATGACACC AGGCTTAAGG TCGACCACGA TGGTTATAAC TACACGCCGT

+2 H S F S G E T D D D N Y L A L S S S K G  
Spacer Region

=====  
2761 GCACAGTTTC TCAGGGGAAA CAGACGATGA CAACTACTTA GCTTTATCAA GCAGTAAAGG  
CGTGTCAAAG AGTCCCCTTT GTCTGCTACT GTTGATGAAT CGAAATAGTT CGTCATTTC

+2 E F L L N G N F V V T M A K R E I R I G  
Spacer Region

=====  
2821 TGAATTCTTG CTAAATGGAA ACTTTGTTGT CACAATGGCC AAAAGGGAAA TTCGCATTGG  
ACTTAAGAAC GATTTACCTT TGAAACAACA GTGTACC GG TTTCCCTTT AAGCGTAACC

+2 N A V V E Y S G S E T A V E R I N S T C  
Spacer Region

=====  
2881 GAATGCTGTG GTAGAGTACA GTGGGTCCGA GACTGCCGTA GAAAGAATTA ACTCAACAGA  
CTTACGACAC CATCTCATGT CACCCAGGCT CTGACGGCAT CTTTCTTAAT TGAGTTGTCT

+2 R I E Q E L L L Q V L S V G K L Y N P D  
Spacer Region

=====  
2941 TCGCATTGAG CAAGAACTTT TGCTTCAGGT TTTGTCCGTG GGAAAGTTGT ACAACCCCGA  
AGCGTAACTC GTTCTTGAAA ACGAAGTCCA AAACAGCCAC CTTTCAACA TGTTGGGGCT

+2 V R Y S F N I P I E D K P Q Q F Y W N S  
Spacer Region

=====  
3001 TGTACGCTAT TCTTTCAATA TTCCAATTGA AGATAAACCT CAGCAGTTT ACTGGAACAG  
ACATGCGATA AGAAAGTTAT AAGGTAACT TCTATTGGA GTCGTCAAAA TGACCTTGTC

+2 H G P W Q A C S K P C Q G E R K R K L V  
Spacer Region

=====  
3061 TCATGGGCCA TGGCAAGCAT GCAGTAAACC CTGCCAAGGG GAACGGAAAC GAAAACCTTG  
AGTACCCGGT ACCGTTGTA CGTCATTGG GACGGTCCCC CTGCGCTTG CTTTGAACA

+2 C T R E S D Q L T V S D Q R C D R L P C  
Spacer Region

=====  
3121 TTGCACCAGG GAATCTGATC AGCTTACTGT TTCTGATCAA AGATGCGATC GGCTGCCCA  
AACGTGGTCC CTTAGACTAG TCGAATGACA AAGACTAGTT TCTACGCTAG CCGACGGGGT

+2 P G H I T E P C G T D C D L R W H V A S  
Spacer Region

=====  
3181 GCCTGGACAC ATTACTGAAC CCTGTGGTAC AGACTGTGAC CTGAGGTGGC ATGTTGCCAG  
CGGACCTGTG TAATGACTTG GGACACCATG TCTGACACTG GACTCCACCG TACAACGGTC

3181 GCCTGGACAC ATTACTGAAC CCTGTGGTAC AGACTGTGAC CTGAGGTGGC ATGTTGCCAG  
CGGACCTGTG TAATGACTTG GGACACCATG TCTGACACTG GACTCCACCG TACAACGGTC

```

+2  R S E C S A Q C G L G Y R T L D I Y C A
    Spacer Region
=====
3241 CAGGAGTGAA TG TAGTGCCC AGTGTGGCTT GGGTTACCGC ACATTGGACA TCTACTGTGC
    GTCCTCACTT ACATCACGGG TCACACCGAA CCCAATGGCG TGTAACCTGT AGATGACACG

+2  K Y S R L D G K T E K V D D G F C S S H
    Spacer Region
=====
3301 CAAATATAGC AGGCTGGATG GGAAGACTGA GAAGGTTGAT GATGGTTTTT GCAGCAGCCA
    GTTTATATCG TCCGACCTAC CCTTCTGACT CTTCCAATA CTACCAAAAA CGTCGTCGGT

+2  P K F S N R E K C S G E C N T G G W R Y
    Spacer Region
=====
3361 TCCCAAACCA AGCAACCGTG AAAAATGCTC AGGGGAATGT AACACGGGTG GCTGGCGCTA
    AGGGTTTGGT TCGTTGGCAC TTTTACGAG TCCCCTTACA TTGTGCCAC CGACCGCGAT

+2  S A W T E C S K S C D G G T Q R R R A I
    Spacer Region
=====
3421 TTCTGCCTGG ACTGAATGTT CAAAAGCTG TGACGGTGGG ACCCAGAGGA GAAGGGCTAT
    AAGACGGACC TGAATTACAA GTTTTTCGAC ACTGCCACCC TGGGTCTCCT CTTCCCGATA

+2  C V N T R N D V L D D S K C T H Q E K V
    TSP2
=====
3481 TTGTGTCAAT ACCCGAAATG ATGTACTGGA TGACAGCAAA TGCACACATC AAGAGAAAGT
    AACACAGTTA TGGGCTTTAC TACATGACCT ACTGTGTTT ACGTGTGTAG TTCTCTTTCA

+2  T I Q R C S E F P C P Q W K S G D W S E
    TSP2
=====
3541 TACCATTAG AGGTGCAGTG AGTTCCCTTG TCCACAGTGG AAATCTGGAG ACTGGTCAGA
    ATGGTAAGTC TCCACGTCAC TCAAGGGAAC AGGTGTCACC TTTAGACCTC TGACCAGTCT

+2  C L V T C G K G H K H R Q V W C Q F G E
    TSP3
=====
3601 GTGCTTGGTC ACCTGTGGAA AAGGGCATAA GCACCGCCAG GTCTGGTGTC AGTTTGGTGA
    CACGAACCAG TGGACACCTT TTCCCGTATT CGTGGCGGTC CAGACCACAG TCAAACCACT

+2  D R L N D R M C D F E T K P T S M Q T C
    TSP3
=====
3661 AGATCGATTA AATGATAGAA TGTGTGACCC TGAGACCAAG CCAACATCTA TGCAGACTTG
    TCTAGCTAAT TTAATATCTT ACACACTGGG ACTCTGGTTC GGTGTAGAT ACGTCTGAAC

+2  Q Q F E C A S W Q A G P W G Q C S V T C
    TSP3
=====
3721 TCAGCAGCCG GAATGTGCAT CCTGGCAGGC GGGTCCCTGG GGACAGTGCA GTGTCACTTG
    AGTCGTCGGC CTTACACGTA GGACCGTCCG CCCAGGGACC CCTGTCACGT CACAGTGAAC

```

```

      G Q G Y Q L R A V K C I I G T Y M S V V
      TSP4
=====
3781  TGGACAGGGA TACCAGCTAA GAGCAGTGAA ATGCATCATT GGGACTTATA TGTCAGTGGT
      ACCTGTCCCT ATGGTCGATT CTCGTCACTT TACGTAGTAA CCCTGAATAT ACAGTCACCA

+2   D D N D C N A A T R P T D T Q D C E L F
      TSP4
=====
3841  AGATGACAAT GACTGTAATG CAGCAACTAG ACCAACTGAT ACCCAGGACT GTGAATTACC
      TCTACTGTTA CTGACATTAC GTCGTTGATC TGGTTGACTA TGGGTCTCTGA CACTTAATGG

+2   S C H P P P A A P E T R R S T Y S A P R
      TSP4
=====
3901  ATCATGTCAT CCTCCCCCAG CTGCCCCGGA AACGAGGAGA AGCACATACA GTGCACCAAG
      TAGTACAGTA GGAGGGGGTC GACGGGGCCT TTGCTCCTCT TCGTGTATGT CACGTGGTTC

+2   T Q W R F G S W T P C S A T C G K G T R
      TSP5
=====
3961  AACCCAGTGG CGATTGGGT CTTGGACCCC ATGCTCAGCC ACTTGTGGGA AAGGTACCCG
      TTGGGTCAAC GCTAAACCCA GAACCTGGGG TACGAGTCGG TGAACACCCT TTCCATGGGC

+2   M R Y V S C R D E N G S V A D E S A C A
      TSP5
=====
4021  GATGAGATAC GTCAGCTGCC GAGATGAGAA TGGCTCTGTG GCTGACGAGA GTGCCTGTGC
      CTACTCTATG CAGTCGACGG CTCTACTCTT ACCGAGACAC CGACTGCTCT CACGGACACG

+2   T L P R P V A K E E C S V T P C G Q W K
      TSP5
=====
4081  TACCCTGCCT AGACCAGTGG CAAAGGAAGA ATGTTCTGTG ACACCCTGTG GGCAATGGAA
      ATGGGACGGA TCTGGTCACC GTTCTCTTCT TACAAGACAC TGTTGGGACAC CCGTTACCTT

+2   A L D W S S C S V T C G Q G R A T R Q V
      TSP6
=====
4141  GGCCTTGGAC TGGAGCTCTT GCTCTGTGAC CTGTGGGCAA GGTAGGGCAA CCCGGCAAGT
      CCGGAACCTG ACCTCGAGAA CGAGACACTG GACACCCGTT CCATCCCGTT GGGCCGTTCA

+2   M C V N Y S D H V I D R S E C D Q D Y I
      TSP6
=====
4201  GATGTGTGTC AACTACAGTG ACCACGTGAT CGATCGGAGT GAGTGTGACC AGGATTATAT
      CTACACACAG TTGATGTCAC TGGTGCAC TA GCTAGCCTCA CTCACACTGG TCCTAATATA

+2   P E T D Q D C S M S P C P Q R T P D S G
      TSP6
=====
4261  CCCAGAAACT GACCAGGACT GTTCCATGTC ACCATGCCCT CAAAGGACCC CAGACAGTGG
      GGGTCTTTGA CTGGTCTCTGA CAAGGTACAG TGGTACGGGA GTTTCCTGGG GTCTGTCAAC

```



```

=====
4861 CCTGGCTAAG CCACATGGGC ACAGAAAGTG CCGAGGAGGA AGATGCCCCA AATGGAAAGC
GGACCGATTG GGTGTACCCG TGTCTTTCAC GGCTCCTCCT TCTACGGGGT TTACCTTTCC

+2 G A W S Q C S V S C G R G V Q Q R H V G
TSP10

=====
4921 TGGCGCTTGG AGTCAGTGCT CTGTGTCCTG TGGCCGAGGC GTACAGCAGA GGCATGTGGG
ACCGCGAACC TCAGTCACGA GACACAGGAC ACCGGCTCCG CATGTCGTCT CCGTACACCC

+2 C Q I G T H K I A R E T E C N P Y T R F
TSP10

=====
4981 CTGTCAGATC GGAACACACA AAATAGCCAG AGAGACCGAG TGCAACCCAT ACACCAGACC
GACAGTCTAG CCTTGTGTGT TTTATCGGTC TCTCTGGCTC ACGTTGGGTA TGTGGTCTGG

+2 E S E R D C Q G P R C P L Y T W R A E E
TSP10 TSP11

=====
5041 GGAGTCGGAA CGCGACTGCC AAGGCCACG GTGTCCCCTC TACACTTGGA GGGCAGAGGA
CCTCAGCCTT GCGCTGACGG TTCCGGGTGC CACAGGGGAG ATGTGAACCT CCCGTCTCCT

+2 W Q E C T K T C G E G S R Y R K V V C V
TSP11

=====
5101 ATGGCAAGAA TGCACCAAGA CCTGCGGCGA AGGCTCCAGG TACCGCAAGG TGGTGTGTGT
TACCGTTCCT ACGTGGTTCT GGACGCCGCT TCCGAGGTCC ATGGCGTTCC ACCACACACA

+2 D D N K N E V H G A R C D V S K R P V D
TSP11

=====
5161 GGATGACAAC AAAAACGAGG TGCAATGGGC ACGCTGTGAC GTGAGCAAGC GGCCGGTGGG
CCTACTGTTG TTTTGTCTCC ACGTACCCCG TCGGACACTG CACTCGTTCC CCGGCCACCT

+2 R E S C S L Q P C E Y V W I T G E W S E
TSP11

=====
5221 CCGTGAAAGC TGAGTTTGC AACCTGCGA GTATGTCTGG ATCACAGGAG AATGGTCAGA
GGCACTTTCC ACATCAAACG TTGGGACGCT CACACAGACC TAGTGTCTTC TTACCACTCT

+2 V P S W E L *
Termination codon
=====
5281 GGTACCGTCC TGGGAAGTGT AACCATCGTC AGCTCAGCCA TGGCCTGAGA GTGGCAGAGG
CCAATGGCAGG ACCCTTGACA TTGGTAGCAG TCGAGTCGGT ACCGGACTCT CACCGTCTCC

5341 GATGAGTGGG GGGATGAGTG CAGGAATGTG GGAGACTTGA GGCTACCCGC CCGATTGTCC
CTACTCACCT CCTACTCAC GTCTTACAC CCTCTGAACT CCGATGGGCG GGCTAAACGG

5401 ACTGTGAACT GTGTGTTTTC TGACAAGTCC TCAGCTTTCC CAAGCTAGAA TTCCTTGTAT
TGACACTTGA CACACAAAAG ACTGTTCAGG AGTCGAAAGG GTTCGATCTT AAGGAACATA

5461 GCAAAGCGGG AGAGATGTAA GAGATGGTCT CTAAGTCCCT TCAGGTCTAC ATTCTGTGAT
CGTTTCGCCC TCTCTACATT CTCTACCAGA GATTCAGGGA AGTCCAGATG TAAGACACTA

```

5521 TCACCTTGAT GTCCTATTGG CATAAAGAAG AAATTATTAC AGGGGCTGCA AACTCATAGG  
 AGTGGAACTA CAGGATAACC GTATTTCTTC TTAAATAATG TCCCCGACGT TTGAGTATCC  
  
 5581 ATGCTGTGAG GTGCCTGAAG ACAGTTAAGT ATAAGAAAAT ATTGTAGTGC CAGGGATACA  
 TACGACACTC CACGGACTTC TGTCAATTCA TATTCTTTTA TAACATCAGG GTCCCTATGT  
  
 5641 ACAAGGAGAG ATGGCAACTG TGACAACTA GCACATGCTG TGTGAAGGGA GCAGAATCTC  
 TGTTCCTCTC TACCGTTGAC ACTGTTTGAT CGTGACGAC ACACTTCCTT CGTCTTAGAG  
  
 5701 TTTCACTCCA GCTGTGGCCA TGCAGAAATG TGGTCTAGCG TTACCAGACC TGATTTTTC  
 AAAGTGAGGT CGACACCGGT ACGTCTTAC ACCAGATCGC AATGGTCTGG ACTAAAAAGT  
  
 5761 AGAGAGGCTA AAAATCTGGA CTAGTATGTG AGATTTCTTA ACTTGAAAAT GGGGGCTGAA  
 TCTCTCCGAT TTTTAGACCT GATCATACAC TCTAAAGGAT TGAACTTTTA CCCCCGACTT  
  
 5821 ATTTTTGGTT TTAAACATT GTAAGGGGCA AACAAACCCC TTTCATGAAC CAGATGTGT  
 TAAAAACCAA AATTTTGTA CATTCCCCGT TTGTTTGGG AAAGTACTTG GTCTACACAA  
  
 5881 GTGCCTGTTT AACAAACAGC TTCAGAGGAA GAAAATAATT TTCTATAATA TCCGAAGTAT  
 CACGGACAAA TTGTTTGTG AAGTCTCCTT CTTTTATTAA AAGATATTAT AGGCTTCATA  
  
 5941 CTCAAGTACC ATTTTTTCAT ATATCTTCCT GTGCACAATG CTTATCTAGA CCCTTTTAA  
 GAGTTCAIGG TAAAAAGTA TATAGAAGGA CACGTGTTAC GAATAGATCT GGGAAAAAT

PolyA Site

=====

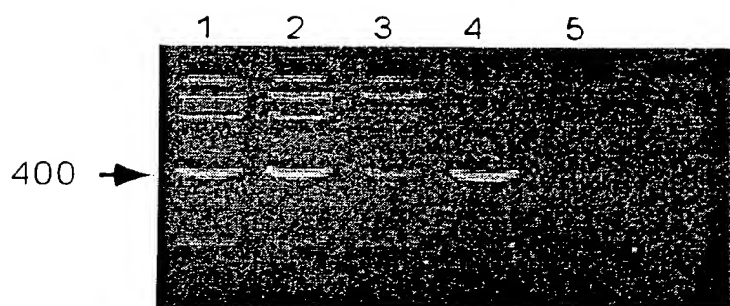
6001 TGGTAATAAA CCAGTAGTAA TCAT  
 ACCATTATTT GGTTCATCATT AGTA

Percent Homology (SI vs)	Ident
Sim	

[illegible]

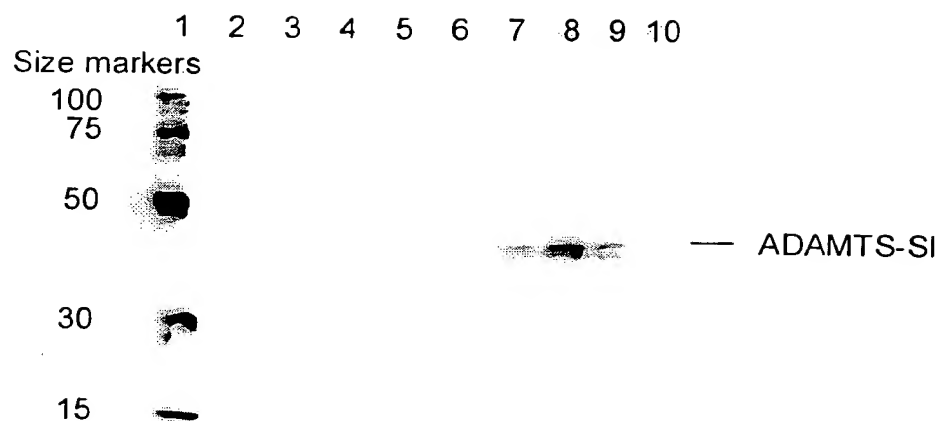


FIG 5



2025001 29122660

Figure 6



Lane 1 His Ladder (Qiagen)  
 Lane 2 Empty well  
 Lane 3 Total lysate  
 Lane 4 Unbound material  
 Lane 5 Wash material  
 Lane 6 50 mM Imidazole Eluate  
 Lane 7 100 mM Imidazole Eluate  
 Lane 8 250 mM Imidazole Eluate  
 Lane 9 2nd 250 mM Imidazole Eluate  
 Lane 10 Ni-NTA resin

FIG. 7

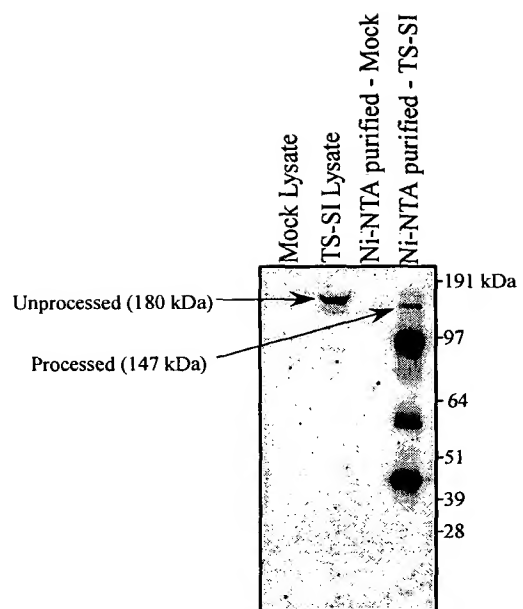
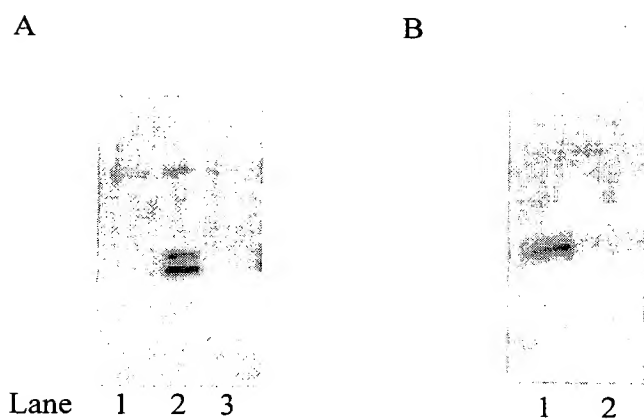


FIG. 8



Western Blot analysis of ADAMTS-4 and ADAMTS-SI cleavage of aggrecanase substrate. A, lane 1 = uncleaved substrate, lane 2 = ADAMTS-4, lane 3 = ADAMTS-4 + 1  $\mu$ M compound I. B, lane 1 = ADAMTS-SI and lane 2 = ADAMTS-SI + 1  $\mu$ M compound I.